

SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

<120> TRANSPORTER GENES

<130> C2-906DP1PCT

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<150> JP 9-260972
JP 10-156660

<151> 1997-9-8
1998-5-20

<160> 28

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<211> 551

<212> PRT

<213> Homo sapiens

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1 5

Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
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Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
30 35 40

Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
45 50 55

Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
60 65 70

Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
75 80 85

Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu

SubA1

002030-507550

90 95 100 105
 Gly Gln Leu Glu Gln Glu Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln
 110 115 120
 Asp Val Tyr Leu Ser Thr Val Val Thr Glu Trp Asn Leu Val Cys Glu
 125 130 135
 Asp Asn Trp Lys Val Pro Leu Thr Thr Ser Leu Phe Phe Val Gly Val
 140 145 150
 Leu Leu Gly Ser Phe Val Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg
 155 160 165
 Lys Asn Val Leu Phe Ala Thr Met Ala Val Gln Thr Gly Phe Ser Phe
 170 175 180 185
 Leu Gln Ile Phe Ser Ile Ser Trp Glu Met Phe Thr Val Leu Phe Val
 190 195 200
 Ile Val Gly Met Gly Gln Ile Ser Asn Tyr Val Val Ala Phe Ile Leu
 205 210 215
 Gly Thr Glu Ile Leu Gly Lys Ser Val Arg Ile Ile Phe Ser Thr Leu
 220 225 230
 Gly Val Cys Thr Phe Phe Ala Val Gly Tyr Met Leu Leu Pro Leu Phe
 235 240 245
 Ala Tyr Phe Ile Arg Asp Trp Arg Met Leu Leu Leu Ala Leu Thr Val
 250 255 260 265
 Pro Gly Val Leu Cys Val Pro Leu Trp Trp Phe Ile Pro Glu Ser Pro
 270 275 280
 Arg Trp Leu Ile Ser Gln Arg Arg Phe Arg Glu Ala Glu Asp Ile Ile
 285 290 295
 Gln Lys Ala Ala Lys Met Asn Asn Thr Ala Val Pro Ala Val Ile Phe
 300 305 310
 Asp Ser Val Glu Glu Leu Asn Pro Leu Lys Gln Gln Lys Ala Phe Ile
 315 320 325

Sub A1

00449-03000

Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser
330 335 340 345

Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu
350 355 360

Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser
365 370 375

Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Arg
380 385 390

Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly
395 400 405

Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu
410 415 420 425

Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe
430 435 440

Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg
445 450 455

Asn Met Ala Val Gly Val Thr Ser Thr Ala Ser Arg Val Gly Ser Ile
460 465 470

Ile Ala Pro Tyr Phe Val Tyr Leu Gly Ala Tyr Asn Arg Met Leu Pro
475 480 485

Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu
490 495 500 505

Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln
510 515 520

Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser
525 530 535

Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe
540 545 550

Sub A1

002020-030700

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 <213> Homo sapiens

<220>
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 caagtttcgg agcggcagtg ggaagc atg cgg gac tac gac gag gtg atc gcc 173
 Met Arg Asp Tyr Asp Glu Val Ile Ala
 1 5
 ttc ctg ggc gag tgg ggg ccc ttc cag cgc ctc atc ttc ttc ctg ctc 221
 Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
 10 15 20 25
 agc gcc agc atc atc ccc aat ggc ttc aat ggt atg tca gtc gtg ttc 269
 Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
 30 35 40
 ctg gcg ggg acc ccg gag cac cgc tgt cga gtc ccg gac gcc gcg aac 317
 Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
 45 50 55
 ctg agc agc gcc tgg cgc aac aac agt gtc ccg ctg cgg ctg cgg gac 365
 Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
 60 65 70
 ggc cgc gag gtg ccc cac agc tgc agc cgc tac cgg ctc gcc acc atc 413
 Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
 75 80 85
 gcc aac ttc tcg gcg ctc ggg ctg gag ccg ggg cgc gac gtg gac ctg 461
 Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu
 90 95 100 105
 ggg cag ctg gag cag gag agc tgc ctg gat ggc tgg gag ttc agc cag 509

Sub A17

0040300-507500

Gly Gln Leu Glu Gln Glu Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln
 110 115 120
 gac gtc tac ctg tcc acc gtc gtg acc gag tgg aat ctg gtg tgt gag 557
 Asp Val Tyr Leu Ser Thr Val Val Thr Glu Trp Asn Leu Val Cys Glu
 125 130 135
 gac aac tgg aag gtg ccc ctc acc acc tcc ctg ttc ttc gta ggc gtg 605
 Asp Asn Trp Lys Val Pro Leu Thr Thr Ser Leu Phe Phe Val Gly Val
 140 145 150
 ctc ctc ggc tcc ttc gtg tcc ggg cag ctg tca gac agg ttt ggc agg 653
 Leu Leu Gly Ser Phe Val Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg
 155 160 165
 aag aac gtt ctc ttc gca acc atg gct gta cag act ggc ttc agc ttc 701
 Lys Asn Val Leu Phe Ala Thr Met Ala Val Gln Thr Gly Phe Ser Phe
 170 175 180 185
 ctg cag att ttc tcc atc agc tgg gag atg ttc act gtg tta ttt gtc 749
 Leu Gln Ile Phe Ser Ile Ser Trp Glu Met Phe Thr Val Leu Phe Val
 190 195 200
 atc gtg ggc atg ggc cag atc tcc aac tat gtg gta gcc ttc ata cta 797
 Ile Val Gly Met Gly Gln Ile Ser Asn Tyr Val Val Ala Phe Ile Leu
 205 210 215
 gga aca gaa att ctt ggc aag tca gtt cgt att ata ttc tct aca tta 845
 Gly Thr Glu Ile Leu Gly Lys Ser Val Arg Ile Ile Phe Ser Thr Leu
 220 225 230
 gga gtg tgc aca ttt ttt gca gtt ggc tat atg ctg ctg cca ctg ttt 893
 Gly Val Cys Thr Phe Phe Ala Val Gly Tyr Met Leu Leu Pro Leu Phe
 235 240 245
 gct tac ttc atc aga gac tgg cgg atg ctg ctg ctg gcg ctg acg gtg 941
 Ala Tyr Phe Ile Arg Asp Trp Arg Met Leu Leu Leu Ala Leu Thr Val
 250 255 260 265
 ccg gga gtg ctg tgt gtc ccg ctg tgg tgg ttc att cct gaa tct ccc 989
 Pro Gly Val Leu Cys Val Pro Leu Trp Trp Phe Ile Pro Glu Ser Pro
 270 275 280

SubA1

004000-000000

cga tgg ctg ata tcc cag aga aga ttt aga gag gct gaa gat atc atc	1037
Arg Trp Leu Ile Ser Gln Arg Arg Phe Arg Glu Ala Glu Asp Ile Ile	
285 290 295	
caa aaa gct gca aaa atg aac aac aca gct gta cca gca gtg ata ttt	1085
Gln Lys Ala Ala Lys Met Asn Asn Thr Ala Val Pro Ala Val Ile Phe	
300 305 310	
gat tct gtg gag gag cta aat ccc ctg aag cag cag aaa gct ttc att	1133
Asp Ser Val Glu Glu Leu Asn Pro Leu Lys Gln Gln Lys Ala Phe Ile	
315 320 325	
ctg gac ctg ttc agg act cgg aat att gcc ata atg acc att atg tct	1181
Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser	
330 335 340 345	
ttg ctg cta tgg atg ctg acc tca gtg ggt tac ttt gct ctg tct ctg	1229
Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu	
350 355 360	
gat gct cct aat tta cat gga gat gcc tac ctg aac tgt ttc ctc tct	1277
Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser	
365 370 375	
gcc ttg att gaa att cca gct tac att aca gcc tgg ctg cta ttg cga	1325
Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Leu Arg	
380 385 390	
acg ctg ccc agg cgt tat atc ata gct gca gta ctg ttc tgg gga gga	1373
Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly	
395 400 405	
ggt gtg ctt ctc ttc att caa ctg gta cct gtg gat tat tac ttc tta	1421
Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu	
410 415 420 425	
tcc att ggt ctg gtc atg ctg gga aaa ttt ggg atc acc tct gct ttc	1469
Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe	
430 435 440	
tcc atg ctg tat gtc ttc act gct gag ctc tac cca acc ctg gtc agg	1517
Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg	
445 450 455	

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 Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro
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 Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu
 35 40 45
 His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg
 50 55 60
 Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His
 65 70 75
 Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu
 80 85 90 95
 Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu
 100 105 110
 Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr
 115 120 125
 Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro
 130 135 140
 Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile
 145 150 155
 Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val
 160 165 170 175
 Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys
 180 185 190
 Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln
 195 200 205
 Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly
 210 215 220
 Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr

SUBA17

002020-002020

225						230						235					
Ala	Phe	Gly	Tyr	Met	Val	Leu	Pro	Leu	Phe	Ala	Tyr	Phe	Ile	Arg	Asp		
240					245					250					255		
Trp	Arg	Met	Leu	Leu	Val	Ala	Leu	Thr	Met	Pro	Gly	Val	Leu	Cys	Val		
			260						265					270			
Ala	Leu	Trp	Trp	Phe	Ile	Pro	Glu	Ser	Pro	Arg	Trp	Leu	Ile	Ser	Gln		
		275						280					285				
Gly	Arg	Phe	Glu	Glu	Ala	Glu	Val	Ile	Ile	Arg	Lys	Ala	Ala	Lys	Ala		
	290						295					300					
Asn	Gly	Ile	Val	Val	Pro	Ser	Thr	Ile	Phe	Asp	Pro	Ser	Glu	Leu	Gln		
305						310					315						
Asp	Leu	Ser	Ser	Lys	Lys	Gln	Gln	Ser	His	Asn	Ile	Leu	Asp	Leu	Leu		
320					325					330					335		
Arg	Thr	Trp	Asn	Ile	Arg	Met	Val	Thr	Ile	Met	Ser	Ile	Met	Leu	Trp		
			340						345					350			
Met	Thr	Ile	Ser	Val	Gly	Tyr	Phe	Gly	Leu	Ser	Leu	Asp	Thr	Pro	Asn		
			355					360					365				
Leu	His	Gly	Asp	Ile	Phe	Val	Asn	Cys	Phe	Leu	Ser	Ala	Met	Val	Glu		
	370						375					380					
Val	Pro	Ala	Tyr	Val	Leu	Ala	Trp	Leu	Leu	Leu	Gln	Tyr	Leu	Pro	Arg		
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Arg	Tyr	Ser	Met	Ala	Thr	Ala	Leu	Phe	Leu	Gly	Gly	Ser	Val	Leu	Leu		
400				405						410					415		
Phe	Met	Gln	Leu	Val	Pro	Pro	Asp	Leu	Tyr	Tyr	Leu	Ala	Thr	Val	Leu		
			420					425					430				
Val	Met	Val	Gly	Lys	Phe	Gly	Val	Thr	Ala	Ala	Phe	Ser	Met	Val	Tyr		
		435					440					445					
Val	Tyr	Thr	Ala	Glu	Leu	Tyr	Pro	Thr	Val	Val	Arg	Asn	Met	Gly	Val		
	450					455						460					

aat ggc ttc acc ggc ctg tcc tcc gtg ttc ctg ata gcg acc ccg gag 264
Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu

35 40 45
 cac cgc tgc egg gtg ccg gac gcc gcg aac ctg agc agc gcc tgg cgc 312
 His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg
 50 55 60
 aac cac act gtc cca ctg cgg ctg cgg gac ggc cgc gag gtg ccc cac 360
 Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His
 65 70 75
 agc tgc cgc cgc tac cgg ctc gcc acc atc gcc aac ttc tgc gcg ctc 408
 Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu
 80 85 90 95
 ggg ctg gag ccg ggg cgc gac gtg gac ctg ggg cag ctg gag cag gag 456
 Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu
 100 105 110
 agc tgt ctg gat ggc tgg gag ttc agt cag gac gtc tac ctg tcc acc 504
 Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr
 115 120 125
 att gtg acc gag tgg aac ctg gtg tgt gag gac gac tgg aag gcc cca 552
 Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro
 130 135 140
 ctc aca atc tcc ttg ttc ttc gtg ggt gtg ctg ttg ggc tcc ttc att 600
 Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile
 145 150 155
 tca ggg cag ctg tca gac agg ttt ggc cgg aag aat gtg ctg ttc gtg 648
 Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val
 160 165 170 175
 acc atg ggc atg cag aca ggc ttc agc ttc ctg cag atc ttc tgc aag 696
 Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys
 180 185 190
 aat ttt gag atg ttt gtc gtg ctg ttt gtc ctt gta ggc atg ggc cag 744
 Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln
 195 200 205
 atc tcc aac tat gtg gca gca ttt gtc ctg ggg aca gaa att ctt ggc 792

Sub A1

002020-5012560

Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly
 210 215 220

aag tca gtt cgt ata ata ttc tct acg tta gga gtg tgc ata ttt tat 840
 Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr
 225 230 235

gca ttt ggc tac atg gtg ctg cca ctg ttt gct tac ttc atc cga gac 888
 Ala Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp
 240 245 250 255

tgg cgg atg ctg ctg gtg gcg ctg acg atg ccg ggg gtg ctg tgc gtg 936
 Trp Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val
 260 265 270

gca ctc tgg tgg ttc atc cct gag tcc ccc cga tgg ctc atc tct cag 984
 Ala Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln
 275 280 285

gga cga ttt gaa gag gca gag gtg atc atc cgc aag gct gcc aaa gcc 1032
 Gly Arg Phe Glu Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ala
 290 295 300

aat ggg att gtt gtg cct tcc act atc ttt gac ccg agt gag tta caa 1080
 Asn Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln
 305 310 315

gac cta agt tcc aag aag cag cag tcc cac aac att ctg gat ctg ctt 1128
 Asp Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu
 320 325 330 335

cga acc tgg aat atc cgg atg gtc acc atc atg tcc ata atg ctg tgg 1176
 Arg Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp
 340 345 350

atg acc ata tca gtg ggc tat ttt ggg ctt tcg ctt gat act cct aac 1224
 Met Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn
 355 360 365

ttg cat ggg gac atc ttt gtg aac tgc ttc ctt tca gcg atg gtt gaa 1272
 Leu His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu
 370 375 380

SUBA1

002060-5072560

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 Val Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg
 385 390 395
 cgc tat tcc atg gcc act gcc ctc ttc ctg ggt ggc agt gtc ctt ctc 1368
 Arg Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu
 400 405 410 415
 ttc atg cag ctg gta ccc cca gac ttg tat tat ttg gct aca gtc ctg 1416
 Phe Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu
 420 425 430
 gtg atg gtg ggc aag ttt gga gtc acg gct gcc ttt tcc atg gtc tac 1464
 Val Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr
 435 440 445
 gtg tac aca gcc gag ctg tat ccc aca gtg gtg aga aac atg ggt gtg 1512
 Val Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val
 450 455 460
 gga gtc agc tcc aca gca tcc cgc ctg ggc agc atc ctg tct ccc tac 1560
 Gly Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr
 465 470 475
 ttc gtt tac ctt ggt gcc tac gac cgc ttc ctg ccc tac att ctc atg 1608
 Phe Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met
 480 485 490 495
 gga agt ctg acc atc ctg aca gcc atc ctc acc ttg ttt ctc cca gag 1656
 Gly Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu
 500 505 510
 agc ttc ggt acc cca ctc cca gac acc att gac cag atg cta aga gtc 1704
 Ser Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val
 515 520 525
 aaa gga atg aaa cac aga aaa act cca agt cac aca agg atg tta aaa 1752
 Lys Gly Met Lys His Arg Lys Thr Pro Ser His Thr Arg Met Leu Lys
 530 535 540
 gat ggt caa gaa agg ccc aca atc ctt aaa agc aca gcc ttc 1794
 Asp Gly Gln Glu Arg Pro Thr Ile Leu Lys Ser Thr Ala Phe
 545 550 555~~

SubA17

0020ED-5072560

taacatcgct tccagtaagg gagaaactga agaggaa

1831

<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 5

ctaatacgac tcactatagg gc

22

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

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tgtagcgtga agacgacaga a

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 7

tcgagcggcc gcccgggcag gt

22

<210> 8

<211> 22

<212> DNA

<213> Artificial Sequence

SUBA7

004080-5672560

[illegible]

~~<223>~~ Description of Artificial Sequence: Artificial Synthesized Primer Sequence

agggcgtggg gcggagggcg gt

22

<211> 20

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

cttttgagca agttcagcct

20

<211> 24

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

agaggtggct tatgagtatt tctt

24

<211> 22

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

ccagggtttt cccagtcacg ac

22

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 <211> 22
 <212> DNA
 <213> Artificial Sequence

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<210> 13
 <211> 24
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 13
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<210> 14
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 <212> DNA
 <213> Artificial Sequence

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<400> 14
 agctgcatga agagaaggac actg 24

<210> 15
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SUBA17

002020 5072500

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

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agcatcctgt ctccctactt cgtt

24

<210> 16

<211> 33

<212> DNA

<213> Artificial Sequence

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33

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

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<400> 17
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33

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<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

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33

<210> 19

Sub A17

004490-5072560

<211> 33
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 <213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

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33

<210> 20
 <211> 24
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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 20
 cgcgccgaat cgctgaatcc ttcc

24

<210> 21
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 21
 aggcttttga tttgttctgt tgag

24

<210> 22
 <211> 553
 <212> PRT
 <213> Mus musculus

<400> 22
 Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro

Sub A1

007080-587590

1 5 10 15
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 20 25 30
 Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
 35 40 45
 Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
 50 55 60
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
 65 70 75 80
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
 85 90 95
 Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
 115 120 125
 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
 130 135 140
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
 145 150 155 160
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
 165 170 175
 Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
 180 185 190
 Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gly Gln Ile
 195 200 205
 Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220
 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
 225 230 235 240

SubA17

002000-5012500

Ile Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
245 250 255

Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro
260 265 270

Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
275 280 285

Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
290 295 300

Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
305 310 315 320

Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
325 330 335

Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
340 345 350

Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
355 360 365

His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
370 375 380

Pro Ala Tyr Phe Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg
385 390 395 400

Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu
405 410 415

Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val
420 425 430

Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val
435 440 445

Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly
450 455 460

Sub A17

002020 5072560

Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe
465 470 475 480

Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly
485 490 495

Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser
500 505 510

Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg
515 520 525

Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu
530 535 540

Ser Pro Lys Val Leu Ile Thr Ala Phe
545 550

<210> 23

<211> 2083

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (122)..(1780)

<400> 23

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tcgctgaatc ctttctctcc acccacctcc ctcacgcaag ctgaggagga gaggtggaaa 120

c atg cgg gac tac gac gag gtg atc gcc ttc ctg ggc gag tgg ggg ccc 169

Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro

1

5

10

15

ttc cag cgc ctc atc ttc ttt ctg ctc agc gcc agc atc atc ccc aat 217

Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn

20

25

30

ggc ttc aat ggt atg tca gtc gtg ttc ctg gcg ggg acc ccc gag cac 265

Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His

35

40

45

SUB A17

002000-3672560

cgt tgc ctg gtt cct gac act gtg aac ctg agc agc tcc tgg cgc aac 313
 Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
 50 55 60

cac agc atc ccc ttg gag acg aag gac gga cga cag gtg cct cag agc 361
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
 65 70 75 80

tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gcg atg ggg 409
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
 85 90 95

ctg gag cca gga cag gac gtg gat ctg gag cag ctg gag cag gag agc 457
 Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110

tgc ctg gat ggc tgg gag tac gac aag gac atc ttc ctg tcc acc atc 505
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
 115 120 125

gtg aca gag tgg aat ctg gtg tgt gag gat gac tgg aag aca ccc ctc 553
 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
 130 135 140

acc acc tcc ctg ttc ttc gta ggc gtt ctc tgc ggc tcc ttc gtg tct 601
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
 145 150 155 160

ggg cag ctg tca gac agg ttt ggc agg aag aaa gtc ctc ttt gca acc 649
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
 165 170 175

atg gct gtg cag act gga ttc agc ttc gtg cag att ttc tca acc aac 697
 Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
 180 185 190

tgg gag atg ttc act gtg ttg ttt gcc att gtg ggc atg ggc cag atc 745
 Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gly Gln Ile
 195 200 205

tcc aac tac gtg gtg gcc ttc ata cta gga act gaa atc ctg agc aag 793
 Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220

Sub A17

00551405-030700

tgc gtt cgc atc atc ttc tcc aca tta gga gtc tgt aca ttt ttt gca 841
 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
 225 230 235 240

atc ggc tac atg gtc ctg ccg ctg ttt gca tac ttc atc aga gac tgg 889
 Ile Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255

agg atg ctg ctg ctg gcc ctg aca ctg cct ggc ctg ttc tgt gtt ccc 937
 Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro
 260 265 270

ctg tgg tgg ttt att cca gaa tct ccc cgg tgg ctg ata tcc cag agg 985
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
 275 280 285

aga ttt gca gag gcc gaa cag atc atc cag aaa gcc gca aag atg aac 1033
 Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
 290 295 300

agc atc gtg gcg cca gca ggg ata ttc gat cct cta gag cta cag gag 1081
 Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
 305 310 315 320

cta aac tcc ttg aag cag cag aaa gtc ata atc ctg gac ctg ttc agg 1129
 Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
 325 330 335

act cgg aac att gcc acc ata acc gtg atg gct gtg atg ctg tgg atg 1177
 Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
 340 345 350

cta acc tca gtg ggt tac ttt gct ctg tct ctc aat gtt cct aat tta 1225
 Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
 355 360 365

cat gga gat gtc tac ctg aac tgc ttc ctc tct ggc ctg att gaa gtt 1273
 His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
 370 375 380

cca gct tac ttc aca gcc tgg ctg cta ctg cga acc ctg cca cgg aga 1321
 Pro Ala Tyr Phe Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg

Sub A1

002020-5072560

385 390 395 400

tat att ata gct ggg gtg cta ttc tgg gga gga ggt gtg ctt ctc ttg 1369
 Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu
 405 410 415

atc caa gtg gta cct gaa gat tat aac ttt gtg tcc att gga ctg gtg 1417
 Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val
 420 425 430

atg ctg ggg aaa ttt ggg atc acc tct gcc ttc tcc atg ttg tat gtc 1465
 Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val
 435 440 445

ttc act gcg gag ctc tac cca acc ctg gtc agg aac atg gct gtg ggc 1513
 Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly
 450 455 460

atc acc tcc atg gcc tct cgg gtg ggc agc atc att gcc ccc tat ttc 1561
 Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe
 465 470 475

gtt tac ctg ggc gcc tat aac aga ctc cta ccc tac atc ctc atg ggc 1609
 Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly
 485 490 495

agt ctg act gtc ctc att gga atc atc acg ctt ttt ttc cct gaa agt 1657
 Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser
 500 505 510

ttt gga gtg act cta cca gag aac ttg gag cag atg cag aaa gtg aga 1705
 Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg
 515 520 525

ggg ttc aga tgt ggg aaa aaa tca aca gtc tca gtg gac aga gaa gaa 1753
 Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu
 530 535 540

agc ccc aag gtt cta ata act gca ttc taacgagggt tccaaggcac 1800
 Ser Pro Lys Val Leu Ile Thr Ala Phe
 545 550

ttggcaaact gaaaagcaga tgtatacaat gagcagggtg tgatagagca agcctgcaat 1860

SubA1

002030-5612560

cccagcgctc ttgggggtgga gacagaagat caggagttca aggtcatcct tggctacagc 1920

aggagtgtaa gaccagcctg tcttaccaca agcaaccctg tctcaacaga acaaatacaa 1980

agccttttct gctgaaaggg attaacagaa acaatgagca ccaaactgga ctgtggaga 2040

aatgcacact atctcatgaa ttctgggcca ctcttcaga tgg 2083

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 24

cccatgccaa caaggacaaa aagc

24

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 25

acagaacaga aaagccctca gtca

24

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 26

Sub A17

002000-507500

tggttttcgt ggggtgtgctg atgg

<210> 27

<211> 557

<212> PRT

<213> Mus musculus

<400> 27

Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro
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Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
20 25 30

Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
35 40 45

Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
50 55 60

His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
65 70 75 80

Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
85 90 95

Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
100 105 110

Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
115 120 125

Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
130 135 140

Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser
145 150 155 160

Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr
165 170 175

Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn
180 185 190

SUBA17

004030-507550

Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe
405 410 415

[illegible]

Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val
420 425 430

Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val
435 440 445

Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly
450 455 460

Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe
465 470 475 480

Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
485 490 495

Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser
500 505 510

Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
515 520 525

Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp
530 535 540

Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe
545 550 555

<210> 28

<211> 1888

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (60)..(1730)

<400> 28

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atg cgg gac tac gac gag gtg acc gcc ttc cta ggc gag tgg ggg ccc 107
Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro

1

5

10

15

Sub A1

0020E0-96FEE560

ttc cag cgc ctc atc ttc ttc ctg ctc agc gcc agc atc atc ccc aat 155
 Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
 20 25 30

ggc ttc aat ggt atg tcc atc gtg ttc ctg gcg ggg acc ccg gag cac 203
 Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
 35 40 45

cgt tgc ctt gtg cct cac acc gtg aac ctg agc agc gcg tgg cgc aac 251
 Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
 50 55 60

cac agt atc ccg ttg gag acg aag gac gga cga cag gtg cct cag aaa 299
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
 65 70 75 80

tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gag cta ggg 347
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
 85 90 95

ctg gag ccg ggg cgg gac gtg gac ctg gag cag ctg gag cag gag agc 395
 Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110

tgc ctg gat ggc tgg gag tac gac aag gac gtc ttc ctg tcc acc atc 443
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
 115 120 125

gtg aca gag tgg gac ctg gtg tgt aag gat gac tgg aaa gcc cca ctc 491
 Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
 130 135 140

acc acc tcc ttg ttt ttc gtg ggt gtg ctg atg ggc tcc ttc att tca 539
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser
 145 150 155 160

gga cag ctc tca gac agg ttt ggt cgc aag aat gtg ctg ttt ttg acc 587
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr
 165 170 175

atg ggc atg cag act ggc ttc agc ttc ctg cag gtc ttc tct gtg aac 635
 Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn
 180 185 190

SUB A1

004020507550

ttc gag atg ttt aca gtg ctt ttt gtc ctt gtt ggc atg ggt cag atc 683
 Phe Glu Met Phe Thr Val Leu Phe Val Leu Val Gly Met Gly Gln Ile
 195 200 205

tcc aac tac gtg gca gca ttt gtc ctg gga aca gaa att ctt tcc aag 731
 Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220

tca att cga att ata ttc gcc acc tta gga gtt tgc ata ttt tat gcg 779
 Ser Ile Arg Ile Ile Phe Ala Thr Leu Gly Val Cys Ile Phe Tyr Ala
 225 230 235 240

ttt ggc ttc atg gtg ctg cca ctg ttt gca tac ttc atc aga gac tgg 827
 Phe Gly Phe Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255

agg atg ctg ctg ctg gcg ctc act gtg cca ggg gtg cta tgt ggg gct 875
 Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Gly Ala
 260 265 270

ctc tgg tgg ttc atc cct gag tcc cca cga tgg ctc atc tct caa ggc 923
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly
 275 280 285

cga att aaa gag gca gag gtg atc atc cgc aaa gct gcc aaa atc aat 971
 Arg Ile Lys Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ile Asn
 290 295 300

ggg att gtt gca cct tcc act atc ttc gat cca agt gag tta caa gac 1019
 Gly Ile Val Ala Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp
 305 310 315 320

tta aat tct acg aag cct cag ttg cac cac att tat gat ctg atc cga 1067
 Leu Asn Ser Thr Lys Pro Gln Leu His His Ile Tyr Asp Leu Ile Arg
 325 330 335

aca cgg aat atc agg gtc atc acc atc atg tct ata atc ctg tgg ctg 1115
 Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu
 340 345 350

acc ata tca gtg ggc tat ttt gga cta tct ctt gac act cct aac ttg 1163
 Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu

SubA1

002060-5672560

355 360 365
 cat ggg gac atc tat gtg aac tgc ttc cta ctg gcg gct gtt gaa gtc 1211
 His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val
 370 375 380
 cca gcc tat gtg ctg gcc tgg ctg ttg ttg cag tac ttg ccc cgg cga 1259
 Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg
 385 390 395 400
 tat tct atc tgc gct gcc ctt ttc ctg ggt ggc agt gtc ctt ctc ttc 1307
 Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe
 405 410 415
 atg cag ctg gtg cct tca gaa ttg ttt tac ttg tcc act gcc ctg gtg 1355
 Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val
 420 425 430
 atg gtg ggg aag ttt gga atc acc tct gcc tac tcc atg gtc tat gtg 1403
 Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val
 435 440 445
 tac aca gct gag ctg tac ccc act gtg gtc aga aac atg ggt gtg ggg 1451
 Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly
 450 455 460
 gtc agc tcc aca gca tcc cgc ctt ggc agc atc ctg tct ccc tac ttt 1499
 Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe
 465 470 475 480
 gtt tac cta ggt gcc tat gat cgc ttc ctg cct tat att ctc atg gga 1547
 Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
 485 490 495
 agt ctg acc atc ctg aca gct atc ctc acc ttg ttc ttc cct gag agc 1595
 Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser
 500 505 510
 ttt ggt gtc cct ctc cca gat acc att gac cag atg cta agg gtc aaa 1643
 Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
 515 520 525
 gga ata aaa cag tgg caa atc caa agc cag aca aga atg caa aaa gat 1691

SUB A1

000000-56742500

Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp
 530 535 540

Sub A1> ggt gaa gaa agc cca ~~aca~~ gtc cta aag agc aca gcc ttc taacaccctg 1740
 Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe
 545 550 555

tccagaaggc aaaaaactga ttggaaacct tcatgttgtc agaaatgctc tccatgactg 1800

agggtttttc tgttctgtta accttggtgc taacatgctc atggattggg gcatctgtcc 1860

tggagagtca ccttcctcta gggacacc 1888

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SEQ ID NO:29

CTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGT

SEQ ID NO:30

TGTAGCGTGAAGACGACAGAAAGGGCGTGGTGCGGAGGGCGGT

SEQ ID NO:31

acctgcccg

SEQ ID NO:32

accgccctccg

Sub A1

002080-5672560